Troponinindikatoren PCT.ST25 SEQUENCE LISTING

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Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

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Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 545 555 560

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 565 570 575

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 580 585 590

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 595 600 605

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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

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gtgaccgccg	ccgggatcac	tctcggcatg	gacgagctgt	acaagtaa		1908

<210> 8

<211> 635

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnC

Troponinindikatoren PCT.ST25 <400> Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15 Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly 20 25 30 Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 60 Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 140 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 155 160 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 220 Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala 225 230 235 240 Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala 245 250 255 Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys 260 265 270

Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu 275 280 285 Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr 290 295 300 Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu 305 310 315 320 Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile 325 330 335 Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu 340 Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp 355 360 365 Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp 370 380 Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser Lys 385 390 395 400 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp 405 410 415 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly 420 425 430 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly 435 445 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly 450 460 Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe 465 470 475 480 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe 485 490 495 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu 500 510 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 515 520 525 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 530 540 Seite 15

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 545 550 555 560

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 565 570 575

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 580 585 590

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 595 600 605

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 610 620

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 625 630

<210> 9

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnC EF-hand 2, 51-91

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ctgctggagt	tcgtgaccgc	cgcccgcatg	ctaggccaga	accccaccaa	agaggagctg	720
gatgccatca	tcgaggaggt	ggacgaggat	ggcagcggca	ccatcgactt	cgaggagttc	780
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gccctgagca	aagaccccaa	cgagaagcgc	gatcacatgg	tcctgctgga	gttcgtgacc	1500
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210 10						

<210> 10

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnC EF-hand 2, 51-91

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110 Seite 17

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 140 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 220 Val Thr Ala Ala Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu 225 230 240 Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp 245 250 255 Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala 260 265 270 Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 275 280 285 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 290 295 300 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 305 310 315 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His $340 \hspace{1cm} 345$ Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 355 360 365 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 370 380 Seite 18

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Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 385 390 395 400							
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 405 410 415							
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 420 425 430							
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 435 440 445							
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 450 455 460							
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser 465 470 475 480							
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 485 490 495							
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Lys							
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<223> Calcium binding moiety: csTnC - Gly-Gly - csTnI							
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gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420							
aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480 Seite 19							
·							

Troponinindikatoren :PCT.ST25

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<210> 12

<211> 822

<212> PRT

<213> Artificial Sequence

· <220>

<223> Calcium binding moiety: csTnC - Gly-Gly - csTnI

<400> 12

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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly 25 30

Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205 Seite 21

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 220 Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala 225 230 240 Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala 245 250 255 Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys 260 265 270 Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu 275 280 285 Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr 290 300 Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu 305 315 320 Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile 325 330 335 Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu 340 345 350 Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp 355 360 365 Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp 370 380 Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Gly Gly Met Ser 385 390 395 400 Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln His Leu 405 410 415 Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys Glu Ala 420 425 430 Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His Ser Pro 435 440 Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu Ser Lys 450 455 460 Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr Asp Thr 465 470 475 480

Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu Ser Gln 485 490 495 Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg 500 505 510 Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys 515 520 525 His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val Lys Lys 530 540 Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp Trp Arg 545 550 560 Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys Met Phe 565 570 Glu Ala Gly Glu Ser Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe 580 585 590 Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly 595 600 His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly 610 620 Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro 625 630 635 Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala 645 650 Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys Ser Ala Met 660 670 Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly 675 680 Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val 690 700 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile 705 715 720 Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile 725 730 735 Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg 740 750

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His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln 765 765

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr 770 775 780

Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp 785 795 800

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly 805 810 815

Met Asp Glu Leu Tyr Lys . 820

<210> 13

<211> 1959

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 116-135 - Gly-Gly - csTnC <400> atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60 120 ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 180 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240 300 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420 480 aagctggagt acaactacat cagccacaac.gtctatatca ccgccgacaa gcagaagaac ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540 600 gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 660 tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 720 ctgctggagt tcgtgaccgc cgcccgcatg ctcgctgatg ccatgctgcg tgccctgctg 780 ggctccaagc acaaggtcaa cggcggcgcg tcaatgacgg accagcaggc ggaggcccgc gccttcctca gcgaggagat gattgctgag ttcaaagctg cctttgacat gtttgatgcg 840 gacggtggtg gggacatcag caccaaggag ttgggcacgg tgatgaggat gctgggccag 900 960 aaccccacca aagaggagct ggatgccatc atcgaggagg tggacgagga tggcagcggc

Seite 24

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<210> 14

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 116-135 - Gly-Gly - csTnC

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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 90 95 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 140 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 160 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 220 Val Thr Ala Ala Arg Met Leu Ala Asp Ala Met Leu Arg Ala Leu Leu 225 230 240 Gly Ser Lys His Lys Val Asn Gly Gly Ala Ser Met Thr Asp Gln Gln 245 250 255 Ala Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys 265 270 Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Asp Ile Ser Thr 275 280 285 Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys 290 295 300 Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly 305 310 315 Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys 325 330 335

Troponinindikatoren PCT.ST25 Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg 340 345 350 Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly 355 360 Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu 370 380 Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe 385 395 400 Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser 405 410 415 Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu 420 425 430 Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu 445 Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr 450 460 Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr 465 470 480 Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp 485 490 495 Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile $500 \hspace{1.5cm} 505 \hspace{1.5cm} 510$ Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe 515 Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe 530 540 Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn 545 550 560 Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys 565 570 575 Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu 580 585 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu 595 600 Troponinindikatoren PCT.ST25
Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
610 615 620

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala 625 630 635 640

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 645 650

<210> 15

<211> 1827

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 95-131 - Gly-Ser-Gly - csTnC 1-91 <400> atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60 ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180 ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240 cagcacgact tettcaagte egecatgeee gaaggetacg tecaggageg taccatette 300 ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480 ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540 gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600 tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 660 ctgctggagt tcgtgaccgc cgcccgcatg ctagacctga gccagaagct gtttgacctg 720 aggggcaagt tcaagaggcc acctctgcgc cgggtgcgca tgtctgctga tgccatgctg 780 cgtgccctgc tgggctccaa gcacaaggtc ggcagcggca gcatgctaat'ggcgtcaatg 840 acggaccagc aggcggaggc ccgcgccttc ctcagcgagg agatgattgc tgagttcaaa 900 gctgcctttg acatgtttga tgcggacggt ggtggggaca tcagcaccaa ggagttgggc 960 acggtgatga ggatgctggg ccagaacccc accaaagagg agctggatgc catcatcgag 1020 gaggtggacg aggatggcag cggcaccatc gacttcgagg agttcctggt gatgatggtg 1080 cgccagatga aagaggacgc cgagctcatg gtgagcaagg gcgaggagct gttcaccggg 1140 gtggtgccca tcctggtcga gctggacggc gacgtaaacg gccacaagtt cagcgtgtcc 1200 ggcgagggcg agggcgatgc cacctacggc aagctgaccc tgaagttcat ctgcaccacc 1260 Seite 28

ggcaagctgc ccgtgccctg gcccaccctc gtgaccacct tcggctacgg cctgatgtgc	1320
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ggctacgtcc aggagcgcac catcttcttc aaggacgacg gcaactacaa gacccgcgcc	1440
gaggtgaagt tcgagggcga caccctggtg aaccgcatcg agctgaaggg catcgacttc	1500
aaggaggacg gcaacatcct ggggcacaag ctggagtaca actacaacag ccacaacgtc	1 560
tatatcatgg ccgacaagca gaagaacggc atcaaggcca acttcaagat ccgccacaac	1620
atcgaggacg gcagcgtgca gctcgccgac cactaccagc agaacacccc catcggcgac	1680
ggccccgtgc tgctgcccga caaccactac ctgagctacc agtccgccct gagcaaagac	1740
cccaacgaga agcgcgatca catggtcctg ctggagttcg tgaccgccgc cgggatcact	1800
ctcggcatgg acgagctgta caagtaa	1827
•	

<210> 16

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 95-131 - Gly-Ser-Gly - csTnC 1-91 <400> 16

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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly 20 25 30

Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile $35 ext{ } 40 ext{ } 45$

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 140 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 220 Val Thr Ala Ala Arg Met Leu Asp Leu Ser Gln Lys Leu Phe Asp Leu 225 230 240 Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg Val Arg Met Ser Ala 245 250 Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys His Lys Val Gly Ser 260 265 270 Gly Ser Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg 275 280 285 Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp 290 295 300 Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly 305 315 320 Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp 325 330 335 Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe 340 345 Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Glu 355 360 365 Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 370 380 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 385 390 395

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 405 410 415

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 420 425 430

Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met 435 440

Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 450 460

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 465 470 475 480

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 485 490 495

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu 500 505 510

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 515 520 525

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 530 540

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 545 550 555 560

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala 565 570 575

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 580 585 590

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 595 600 605

<210> 17

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 12-161

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Troponinindikatoren PCT.ST25 <400> atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60 ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180 ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300 ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480 ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540 gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600 tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc. 660 ctgctggagt tcgtgaccgc cgcccgcatg ctgctgacag aagagcagaa aaatgagttc 720 aaggcagcct tcgacatctt cgtgctgggc gctgaggatg gctgcatcag caccaaggag 780 ctgggcaagg tgatgaggat gctgggccag aaccccaccc ctgaggagct gcaggagatg 840 atcgatgagg tggacgagga cggcagcggc acggtggact ttgatgagtt cctggtcatg 900 atggttcggt gcatgaagga cgacagcaaa gggaaatctg aggaggagct gtctgacctc 960 ttccgcatgt ttgacaaaaa tgctgatggc tacatcgacc tggatgagct gaagataatg 1020 ctgcaggcta caggcgagac catcacggag gacgacatcg aggaactcat gaaggacgga 1080 1140 gacaagaaca acgacggccg catcgactat gatgagttcc tggagttcat gaagggtgtg gaggagctca tggtgagcaa gggcgaggag ctgttcaccg gggtggtgcc catcctggtc 1200 1260 gagctggacg gcgacgtaaa cggccacaag ttcagcgtgt ccggcgaggg cgagggcgat 1320 gccacctacg gcaagctgac cctgaagttc atctgcacca ccggcaagct gcccgtgccc tggcccaccc tcgtgaccac cttcggctac ggcctgatgt gcttcgcccg ctaccccgac 1380 cacatgcgcc agcacgactt cttcaagtcc gccatgcccg aaggctacgt ccaggagcgc 1440 1500 accatcttct tcaaggacga cggcaactac aagacccgcg ccgaggtgaa gttcgagggc gacaccctgg tgaaccgcat cgagctgaag ggcatcgact tcaaggagga cggcaacatc 1560 ctggggcaca agctggagta caactacaac agccacaacg tctatatcat ggccgacaag 1620 cagaagaacg gcatcaaggc caacttcaag atccgccaca acatcgagga cggcagcgtg 1680 cagctcgccg accactacca gcagaacacc cccatcggcg acggccccgt gctgctgccc 1740 gacaaccact acctgagcta ccagtccgcc ctgagcaaag accccaacga gaagcgcgat 1800 cacatggtcc tgctggagtt cgtgaccgcc gccgggatca ctctcggcat ggacgagctg 1860

tacaagtaa

1869

<211> 622

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 12-161

<400> 18

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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly 20 25 30

Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 220 Seite 33

Val Thr Ala Ala Arg Met Leu Leu Thr Glu Glu Gln Lys Asn Glu Phe 225 230 240 Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile 245 250 255 Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro 260 265 270 Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly 275 280 285 Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met Met Val Arg Cys 290 295 300 Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu 305 310 320 Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu 325 330 335 Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp 340 345 Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile 355 360 365 Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met 370 380 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 385 390 400 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
410
415 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 420 425 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 435 440 445 Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln 450 460 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 465 470 480 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 485 490 495

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly

Tle Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val

545

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser 580 585 590

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 595 600 605

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 610 620

<210> 19

<211> 486

<212> DNA

<213> Homo sapiens

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Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu 35 40 45

Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val 50 60

Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met 65 70 75 80

Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu 90 95

Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile $100 \hspace{1cm} 105 \hspace{1cm} 105$

Asp Leu Asp Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile 115 120 125

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn 130 135

Asp Gly Arg Ile Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val 145 150 155 160

Glu

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<211> 633

<212> DNA

<213> Homo sapiens

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atctccgcct cgagaaaatt gcagctgaag actctgctgc tgcagattgc aaagcaagag 180
Seite 36

240 -

300

360 420

480

540600633

Troponinindikatoren PCT.ST25

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<211> 210
<212> PRT
<213> Homo sapiens
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Pro His Ala Lys Lys Lys Ser Lys Ile Ser Ala Ser Arg Lys Leu Gln 35 40 45
Leu Lys Thr Leu Leu Gln Ile Ala Lys Gln Glu Leu Glu Arg Glu 50 60
Ala Clu Clu Ama Ama Clu Clu Lva Clu Ama Ala Lou San Tha Ama Cua
Ala Glu Glu Arg Arg Gly Glu Lys Gly Arg Ala Leu Ser Thr Arg Cys 65 70 75 80
Gln Pro Leu Glu Leu Thr Gly Leu Gly Phe Ala Glu Leu Gln Asp Leu
85 90 95
Cys Arg Gln Leu His Ala Arg Val Asp Lys Val Asp Glu Glu Arg Tyr
100 105 110
Asp Ile Glu Ala Lys Val Thr Lys Asn Ile Thr Glu Ile Ala Asp Leu
115 120 125
Thr Gln Lys Ile Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Thr Leu
130 135 140
Arg Arg Val Arg Ile Ser Ala Asp Ala Met Met Gln Ala Leu Leu Gly
145 150 155 160

Ala Arg Ala Lys Glu Ser Leu Asp Leu Arg Ala His Leu Lys Gln Val 165 170 175

Lys Lys Glu Asp Thr Glu Lys Glu Asn Arg Glu Val Gly Asp Trp Arg 180 185 190

Lys Asn Ile Asp Ala Leu Sér Gly Met Glu Gly Arg Lys Lys Phe 195 200 205

Glu Ser 210

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<211> 483

<212> DNA

<213> Homo sapiens

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<210> 24

<211> 160

<212> PRT

<213> Homo sapiens

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Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly 20 25 30

<210> 26 <211> 163

ċ212>

Gly Asp Ile Ser Val Lys Glu Leu Glu Leu Glu Asp Glu Asp Gly Ser Gly Thr Ile Asp P Glu Arg Glu Cys Phe Arg Ile Phe Asp Ala Leu Ala Glu Glu Leu Ala Glu Glu Leu Ala Glu Ile Phe Asp Gly Glu Glu Ile Glu Ser Leu Met Leu Ala Gly Arg Ile Asp Phe Asp Glu Phe Leu Ala Gly Arg Ile Asp Phe Asp Glu Phe Leu Ala Gly Arg Ile Asp Phe Asp Glu Phe Leu Ala Gly Arg Ile Asp Phe Asp Glu Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Arg Ile Asp Phe Asp Gly Phe Leu Ala Gly Phe Phe Ala Gly Phe Phe Ala Gly Phe Phe Ala Gly Phe	45 sp Ala Ile Ile Glu Glu Val Asp 60	
Glu Asp Gly Ser Gly Thr Ile Asp P Val Arg Gln Met Lys Glu Asp Ala L Ala Glu Cys Phe Arg Ile Phe Asp A Pro Glu Glu Leu Ala Glu Ile Phe A Asp Glu Glu Ile Glu Ser Leu Met L Gly Arg Ile Asp Phe Asp Glu Phe L 4210> 25 <211> 492	60 he Glu <u>Gl</u> u Phe Leu Val Met Met	
Val Arg Gln Met Lys Glu Asp Ala L Ala Glu Cys Phe Arg Ile Phe Asp A Pro Glu Glu Leu Ala Glu Ile Phe A 115 Asp Glu Glu Ile Glu Ser Leu Met L 130 Gly Arg Ile Asp Phe Asp Glu Phe L 210> 25 2211> 492		
Ala Glu Cys Phe Arg Ile Phe Asp A 100 Pro Glu Glu Leu Ala Glu Ile Phe Asp A 120 Asp Glu Glu Ile Glu Ser Leu Met L 130 Gly Arg Ile Asp Phe Asp Glu Phe L 145 C210> 25 C211> 492	7.5	
Pro Glu Glu Leu Ala Glu Ile Phe A 120 Asp Glu Glu Ile Glu Ser Leu Met L 130 Gly Arg Ile Asp Phe Asp Glu Phe L 150 <210> 25 <211> 492	ys Gly Lys Ser Glu Glu Glu Leu 90 95	
115 120 Asp Glu Glu Ile Glu Ser Leu Met L 130 Gly Arg Ile Asp Phe Asp Glu Phe L 145 <210> 25 <211> 492	rg Asn Ala Asp Gly Tyr Ile Asp 05 110	,
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145 150 <210> 25 <211> 492	ys Asp Gly Asp Lys Asn Asn Asp 140	
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<212> DNA		
<213> Gallus gallus		•
<400> 25		-
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gagattctca gggccactgg ggagcacgtc	atcgaggagg acatagaaga cctcatgaag	420
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ggtgtgcagt aa		492

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<400>	2	6
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Asp Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr Val Met Arg 35 40

Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu 50 60

Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu 65 70 75

. Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu 85 90 95

Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly 100 105

Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr Gly Glu 115 120 125

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Cys Pro Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu 50 60	
	•
Cys Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr 65 70 80	
Asp Thr Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu 85 90 95	
Con Clarky Low Dischar Low Are Clarky Dischar Des Des Low	
Ser Gln Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu 100 105 110	
Arg Arg Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly	
115 120 125	
Ser Lys His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val	
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Lys Lys Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp	
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Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val 50 60

Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met 65 70 75 80

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Troponinindikatoren PCT.ST25 Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Thr Glu Glu 85 90 95

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Asp Leu Glu Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile 115 120 125

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn 130 140

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Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr $50 \hspace{1cm} 55 \hspace{1cm} 60$

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<211> 1866

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Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 75 80	
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	
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Seite 49

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Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 420 425 430

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly 435 440 445

Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His 450 455 460

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 465 470 475 480

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 485 490 495

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp 500 505 510

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr 515 520 525

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile 530 540

Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln 545 550 555 560

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val 565 570 575

Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys 580 585

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<213> Drosophila melanogaster

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<400> 36

Met Ser Asp Glu Leu Thr Lys Glu Gln Thr Ala Leu Leu Arg Asn Ala $1 \hspace{1cm} 5 \hspace{1cm} 15$

Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr Ala Met 20 25 30

Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp Ala Thr 35 40 45

Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly Gln Ile 50 55

Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val Glu Glu 65 70 75 80

Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg Leu Tyr 85 90 95

Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg Glu Ile 100 105 110

Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp Met Met 115 120 125

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Troponinindikatoren PCT.ST25
Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu
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Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp 130 140

Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu 145 150 155

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<213> Drosophila melanogaster

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<400> 40

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Gln Lys Ala Phe Asn Ser Phe Asp His Gln Lys Thr Gly Ser Ile Pro 20 25 30

Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp 35 40 45

Lys Lys Ile Leu Glu Glu Leu Ile Glu Glu Val Asp Glu Asp Lys Ser 50 60

WO 2005/014636 PCT/EP2004/008739

Troponinindikatoren_PCT_ST25 Gly Arg Leu Glu Phe Gly Glu Phe Val Gln Leu Ala Ala Lys Phe Ile 65 70 75 Val Glu Glu Asp Ala Glu Ala Met Gln Lys Glu Leu Ala Glu Ala Phe 85 90 95 Arg Leu Tyr Asp Lys Gln Gly Asn Gly Phe Ile Pro Thr Thr Cys Leu 100 105 110 Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu 115 120 125 Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp 130 140 Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu 145 <210> <211> 1833 <212> DNA <213> Artificial Sequence <220> FRET-pair Cop/Phi; Calcium binding moiety: csTnC 15-163 <223> <400> 60 atgggccccg ccatgaagat cgagtgccgc atcaccggca ccctgaacgg cgtggagttc gagctggtgg gcggcggaga gggcaccccc gagcagggcc gcatgaccaa caagatgaag 120 agcaccaagg gcgccctgac cttcagcccc tacctgctga gccacgtgat gggctacggc 180 ttctaccact tcggcaccta ccccagcggc tacgagaacc ccttcctgca cgccatcaac 240 300 aacggcggct acaccaacac ccgcatcgag aagtacgagg acggcggcgt gctgcacgtg 360 agcttcagct accgctacga ggccggccgc gtgatcggcg acttcaaggt ggtgggcacc 420 ggcttccccg aggacagcgt gatcttcacc gacaagatca tccgcagcaa cgccaccgtg gagcacctgc accccatggg cgataacgtg ctggtgggca gcttcgcccg caccttcagc 480 540 ctgcgcgacg gcggctacta cagcttcgtg gtggacagcc acatgcactt caagagcgcc 600 atccacccca gcatcctgca gaacgggggc cccatgttcg ccttccgccg cgtggaggag ctgcacagca acaccgagct gggcatcgtg gagtaccagc acgccttcaa gaccccgatc 660 gcattcgccc gcatgctcag cgaggagatg attgctgagt tcaaagctgc ctttgacatg 720 780 tttgatgcgg acggtggtgg ggacatcagc accaaggagt tgggcacggt gatgaggatg ctgggccaga accccaccaa agaggagctg gatgccatca tcgaggaggt ggacgaggat 840 900 ggcagcggca ccatcgactt cgaggagttc ctggtgatga tggtgcgcca gatgaaagag

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	ccgaggtgac	t. •	•			1500
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<400> .42

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Gly Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe 35 40

Ser Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe 50 60

Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn 65 70 75 80 Seite 55

Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly 85 90Val Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile 100 105 110 Gly Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile 115 120 125 Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His 130 135 140 Pro Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser 145 150 155 160 Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His 165 170 175Phe Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met 180 185 190 Phe Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly 195 200 205 Ile Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg 210 215 220 Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met 225 230 240 Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr 245 250 255 Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala 260 265 270 Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu 275 280 285 Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly 290 295 300 Lys Ser Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn 305 310 315Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala 325 330 335 Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp 340 345 350

Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys 355 360 365

Met Met Glu Gly Val Gln Glu Leu Met Ser Ser Gly Ala Leu Leu Phe 370 380

His Gly Lys Ile Pro Tyr Val Val Glu Met Glu Gly Asn Val Asp Gly 385 395 400

His Thr Phe Ser Ile Arg Gly Lys Gly Tyr Gly Asp Ala Ser Val Gly 405 410

Lys Val Asp Ala Gln Phe Ile Cys Thr Thr Gly Asp Val Pro Val Pro 420 425 430

Trp Ser Thr Leu Val Thr Thr Leu Thr Tyr Gly Ala Gln Cys Phe Ala 435 440 445

Lys Tyr Gly Pro Glu Leu Lys Asp Phe Tyr Lys Ser Cys Met Pro Asp 450 460

Gly Tyr Val Gln Glu Arg Thr Ile Thr Phe Glu Gly Asp Gly Asn Phe 465 470 470 475 480

Lys Thr Arg Ala Glu Val Thr Phe Glu Asn Gly Ser Val Tyr Asn Arg 485 490 495

Val Lys Leu Asn Gly Gln Gly Phe Lys Lys Asp Gly His Val Leu Gly 500 505 510

Lys Asn Leu Glu Phe Asn Phe Thr Pro His Cys Leu Tyr Ile Trp Gly 515 525

Asp Gln Ala Asn His Gly Leu Lys Ser Ala Phe Lys Ile Cys His Glu 530 540

Ile Thr Gly Ser Lys Gly Asp Phe Ile Val Ala Asp His Thr Gln Met 545 550 555 560

Asn Thr Pro Ile Gly Gly Gly Pro Val His Val Pro Glu Tyr His His 565 570 575

Met Ser Tyr His Val Lys Leu Ser Lys Asp Val Thr Asp His Arg Asp 580 585

Asn Met Ser Leu Lys Glu Thr Val Arg Ala Val Asp Cys Arg Lys Thr 595 600 605

Tyr Leu 610